

(1) GENERAL INFORMATION:

(A) NAME: Max-Planck-Gesellschaft zur Foerderung der
Wissenschaften e.V.

(C) CITY: Berlin

(E) COUNTRY: DE

(F) POSTAL CODE (ZIP): none

(iii) ~~NUMBER OF SEQUENCES: 2.~~

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Tomato

(A) NAME/KEY: CDS

(B) LOCATION: 194..3535

GAAATATTCT TTA~~CTT~~ACTT CACCAGGGAT TGACTCATCA CTCCCTCAA GTCTTTGTGT

120 GTTGTGATAA TAAATTTGGT TGTGCTTCAG TTTCAGTAC TACTGCTGGG TAGTTTTTAT

TTTGATAAC TTCAGGGGGT ATTCCAGTTG GTGTTAGCAT TTGAAAGTCG
AACTGCACTT 180

GGAATTTGGC TAC ATG GGA AAG ACA ATT CAG GTT TTC GGA TTC CCT TAT 229
Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr

1 5 10

CTT CTC TCT GCG GAA GTG GTT AAG TCA TTC TTA GAG AAA TAT ACA GGA	277
Leu Leu Ser Ala Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly	
15 20 25	
TAT GGA ACT GTA TGT GCA TTG GAG GTT AAA CAG TCC AAA GGA GGA TCT	325
Tyr Gly Thr Val Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser	
30 35 40	
AGA GCA TTT GCC AAA GTT CAA TTT GCC GAC AAC ATA AGT GCT GAC AAA	373
Arg Ala Phe Ala Lys Val Gln Phe Ala Asp Asn Ile Ser Ala Asp Lys	
45 50 55 60	
ATC ATC ACT TTG GCT AAT AAC AGG CTG TAT TTT GGC TCT TCT TAT TTG	421
Ile Ile Thr Leu Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu	
65 70 75	
AAG GCT TGG GAA ATG AAA ACT GAT ATT GTC CAA CTG CGG GCA TAT GTG	469
Lys Ala Trp Glu Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val	
80 85 90	
GAT CAG ATG GAT GGC ATA ACT TTG AAT TTC GGA TGT CAG ATA TCA GAT	517
Asp Gln Met Asp Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp	
95 100 105	
GAC AAG TTT GCA GTG TTG GGA AGT ACA GAA GTT TCA ATT CAA TTT GGC	565
Asp Lys Phe Ala Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly	
110 115 120	
ATT GGA TTG AAG AAA TTT TTT TTC TTT TTA TCT AGT GGT TCA GCT GAC	613
Ile Gly Leu Lys Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp	
125 130 135 140	
TAT AAA CTT CAG CTT TCA TAT GAA AAT ATA TGG CAG GTT GTG CTC CAT	661
Tyr Lys Leu Gln Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His	
145 150 155	
CGT CCA TAT GGT CAA AAT GCT CAG TTT CTC CTC ATA CAG TTA TTT GGT	709
Arg Pro Tyr Gly Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly	
160 165 170	
GCT CCT CGG ATC TAT AAG AGA CTT GAA AAC TCC TGT TAT AGC TTC TTT	757
Ala Pro Arg Ile Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe	
175 180 185	
AAG GAA ACT CCT GAT GAT CAG TGG GTG AGG ACA ACA GAT TTC CCT CCA	805
Lys Glu Thr Pro Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro	
190 195 200	
TCT TGG ATA GGG CTA TCT TCT AGC TTA TGT TTG CAG TTC CGT AGG GGT	853
Ser Trp Ile Gly Leu Ser Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly	
205 210 215 220	
GTT CGT CTT CCA AAT TTC GAG GAA AGT TTT TTC CAC TAT GCA GAA CGT	901
Val Arg Leu Pro Asn Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg	
225 230 235	
GAA AAC AAT ATT ACT TTA CAG ACT GGT TTC ACC TTT TTC GTC TCT CAA	949
Glu Asn Asn Ile Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln	

240 245 250
 AAA TCG GCT CTG GTT CCC AAT GTC CAG CCT CCG GAA GGA ATT TCA ATT 997
 Lys Ser Ala Leu Val Pro Asn Val Gln Pro Pro Gln Gly Ile Ser Ile
 255 260 265
 CCC TAC AAG ATT TTG TTC AAA ATT AGT TCT TTG GTA CAG CAT GGA TGC 1045
 Pro Tyr Lys Ile Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys
 270 275 280
 ATA CCT GGG CCA GCA TTA AAT GTC TAC TTT TTC CGA TTA GTT GAT CCT 1093
 Ile Pro Gly Pro Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro
 285 290 295 300
 CGA AGG AGA AAT GTG GCA TGC ATT GAG CAT GCC TTA GAG AAA CTG TAC 1141
 Arg Arg Arg Asn Val Ala Cys Ile Glu His Ala Leu Gln Lys Leu Tyr
 305 310 315
 TAT ATA AAG GAG TGC TGT TAT GAT CCC GTG AGG TGG CTC ACT GAG CAG 1189
 Tyr Ile Lys Gln Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln
 320 325 330
 TAT GAT GGG TAT CTC AAG GGT AGA CAA CCT CCA AAA TCT CCG TCC ATC 1237
 Tyr Asp Gly Tyr Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile
 335 340 345
 ACT TTA GAT GAT GGG TTG GTG TAT GTA AGA AGG GTC CTA GTA ACA CCA 1285
 Thr Leu Asp Asp Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro
 350 355 360
 TGC AAA GTT TAT TTT TGT GGT CCA GAG GTT AAT GTT TCC AAT CGG GTT 1333
 Cys Lys Val Tyr Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val
 365 370 375 380
 CTC CGC AAT TAT TCT GAA GAC ATA GAT AAC TTT CTT CGT GTT TCT TTT 1381
 Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe
 385 390 395
 GTT GAT GAG GAG TGG GAG AAA CTG TAT TCT ACA GAC TTA TTA CCA AAA 1429
 Val Asp Gln Glu Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys
 400 405 410
 GCA AGT ACT GGA AGT GGT GTC AGG ACA AAC ATC TAT GAG AGG ATC TTA 1477
 Ala Ser Thr Gly Ser Gly Val Arg Thr Asn Ile Tyr Gln Arg Ile Leu
 415 420 425
 TCA ACT CTG CGG AAA GGC TTT GTA ATT GGT GAT AAA AAA TTT GAA TTT 1525
 Ser Thr Leu Arg Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe
 430 435 440
 CTT GCA TTT TCA TCG AGC CAG TTG CGG GAT AAT TCA GTG TGG ATG TTT 1573
 Leu Ala Phe Ser Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe
 445 450 455 460
 GCA TCA AGA CCT GGC CTT ACT GCA AAT GAT ATA AGA GCT TGG ATG GGT 1621
 Ala Ser Arg Pro Gly Leu Thr Ala Asn Asp Ile Arg Ala Trp Met Gly
 465 470 475

ACA ATG ATG GGA TGT TTG GAT GAA TCC AGA ACC TTG GAA TAT GGT CAG 2341
Thr Met Met Gly Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln

705	710	715	
GTG TTT GTT CAG TTT ACT GGT GCT GGA CAT GGA GAG TTT TCT GAC GAT	2389		
Val Phe Val Gln Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp			
720 725 730			
TTA CAT CCA TTT AAT AAC AGC AGA TCC ACC AAC AGT AAT TTC ATT CTG	2437		
Leu His Pro Phe Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu			
735 740 745			
AAG GGA AAT GTG GTT GTT GCA AAA AAT CCA TGC TTG CAT CCT GGT GAT	2485		
Lys Gly Asn Val Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp			
750 755 760			
ATT CGT GTT TTA AAG GCT GTA AAT GTT CGA GCG CTG CAC CAC ATG GTA	2533		
Ile Arg Val Leu Lys Ala Val Asn Val Arg Ala Leu His His Met Val			
765 770 775 780			
GAT TGT GTT GTA TTC CCT CAG AAA GGA AAA AGA CCT CAT CCG AAT GAA	2581		
Asp Cys Val Val Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu			
785 790 795			
TGT TCT GGG AGT GAT TTG GAT GGG GAT ATC TAC TTT GTT TGC TGG GAT	2629		
Cys Ser Gly Ser Asp Leu Asp Gly Asp Ile Tyr Phe Val Cys Trp Asp			
800 805 810			
CAA GAC ATG ATC CCG CCA AGG CAA GTC CAG CCG ATG GAA TAT CCT CCA	2677		
Gln Asp Met Ile Pro Pro Arg Gln Val Gln Pro Met Glu Tyr Pro Pro			
815 820 825			
GCA CCC AGC ATA CAG TTG GAC CAT GAT GTC ACA ATT GAG GAA GTT GAA	2725		
Ala Pro Ser Ile Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu			
830 835 840			
GAG TAC TTC ACC AAC TAT ATT GTG AAT GAC AGT TTG GGA ATC ATA GCA	2773		
Glu Tyr Phe Thr Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala			
845 850 855 860			
AAT GCC CAT GTC GTA TTT GCA GAC AGA GAA CCT GAT ATG GCC ATG AGT	2821		
Asn Ala His Val Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser			
865 870 875			
GAT CCA TGC AAA AAA CTT GCT GAG CTC TTT TCA ATT GCA GTG GAC TTT	2869		
Asp Pro Cys Lys Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe			
880 885 890			
CCA AAG ACT GGT GTT CCC GCT GAA ATA CCA TCT CAG TTG CGC CCT AAA	2917		
Pro Lys Thr Gly Val Pro Ala Glu Ile Pro Ser Gln Leu Arg Pro Lys			
895 900 905			
GAA TAC CCA GAC TTC ATG GAT AAG CCG GAC AAG ACC AGC TAT ATC TCA	2965		
Glu Tyr Pro Asp Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser			
910 915 920			
GAA AGA GTT ATT GGA AAG CTT TTC AGG AAA GTG AAG GAC AAA GCA CCT	3013		
Glu Arg Val Ile Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro			
925 930 935 940			

CAG GCT AGC TCT ATC GCG ACC TTC ACA AGA GAT GTT GCA AGG AGA TCA 3061
 Gln Ala Ser Ser Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser
 945 950 955

TAT GAT GCT GAT ATG GAA GTT GAT GGA TTT GAA GAT TAC ATT GAC GAA 3109
 Tyr Asp Ala Asp Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu
 960 965 970

GCT TTT GAC TAC AAA ACT GAA TAT GAC AAC AAG CTG GGT AAT TTA ATG 3157
 Ala Phe Asp Tyr Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met
 975 980 985

GAC TAC TAT GGC ATA AAA ACA GAG GCT GAA ATA CTT AGT GGT GGC ATT 3205
 Asp Tyr Tyr Gly Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile
 990 995 1000

ATG AAG GCA TCA AAA ACT TTT GAC CGC AGA AAA GAT GCT GAG GCC ATT 3253
 Met Lys Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile
 1005 1010 1015 1020

AGT GTT GCT GTG AGG GCC TTG AGG AAG GAG GCA AGA GCC TGG TTC AAG 3301
 Ser Val Ala Val Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys
 1025 1030 1035

AGG CGT AAT GAT ATA GAT GAC ATG TTA CCA AAG GCT TCG GCT TGG TAC 3349
 Arg Arg Asn Asp Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr
 1040 1045 1050

CAC GTT ACA TAT CAT CCT ACA TAT TGG GGT TGC TAC AAT CAG GGG TTG 3397
 His Val Thr Tyr His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu
 1055 1060 1065

AAA AGA GCT CAT TTC ATT AGC TTT CCC TGG TGT GTT TAT GAC CAG CTA 3445
 Lys Arg Ala His Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu
 1070 1075 1080

ATC CAG ATT AAG AAG GAC AAA GCA CGT AAC AGG CCA GTT CTC AAC TTG 3493
 Ile Gln Ile Lys Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu
 1085 1090 1095 1100

TCA TCT CTC AGG GCT CAA CTG AGT CAC AGA TTA GTG TTG AAA 3535
 Ser Ser Leu Arg Ala Gln Leu Ser His Arg Leu Val Leu Lys
 1105 1110

TGAGATTCCA GTCGAGCGTT AAGCTGATAT ATATATAATG TAATAGGGTG
 TGATCATAAG 3595

AAAACTGTTA TGCATTGTTG ACTACCTTTT GTCTTTAAAA CTGCATGAAG CTGCAACATA
 3655

TATGCAGTAC TCTAAGAAAC AGATGTACAG CTAAGTACTA ATATGTATGT
 GATTTGAGTT 3715

TCATCTTTCT TCTAAA 3731

(2) INFORMATION FOR SEQ ID NO: 2:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile Pro Tyr Lys Ile
260 265 270

Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys Ile Pro Gly Pro
275 280 285

Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro Arg Arg Arg Asn
290 295 300

Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr Tyr Ile Lys Glu
305 310 315 320

Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln Tyr Asp Gly Tyr
325 330 335

Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile Thr Leu Asp Asp
340 345 350

Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro Cys Lys Val Tyr
355 360 365

Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val Leu Arg Asn Tyr
370 375 380

Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe Val Asp Glu Glu
385 390 395 400

Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys Ala Ser Thr Gly
405 410 415

Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu Ser Thr Leu Arg
420 425 430

Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe Leu Ala Phe Ser
435 440 445

Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe Ala Ser Arg Pro
450 455 460

Gly Leu Thr Ala Asn Asp Ile Arg Ala Trp Met Gly Asp Phe Ser Gln
465 470 475 480

Ile Lys Asn Val Ala Lys Tyr Ala Ala Arg Leu Gly Gln Ser Phe Gly
485 490 495

Ser Ser Arg Glu Thr Leu Ser Val Leu Arg His Glu Ile Glu Val Ile
500 505 510

Pro Asp Val Lys Val His Gly Thr Ser Tyr Val Phe Ser Asp Gly Ile
515 520 525

Gly Lys Ile Ser Gly Asp Phe Ala His Arg Val Ala Ser Lys Cys Gly
530 535 540

Leu Gln Tyr Thr Pro Ser Ala Phe Gln Ile Arg Tyr Gly Gly Tyr Lys
545 550 555 560

Gly Val Val Gly Val Asp Pro Asp Ser Ser Met Lys Leu Ser Leu Arg
565 570 575

00763374-03333

Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe Pro Lys Thr Gly

895

Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser Glu Arg Val Ile
915 920 925

Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro Gln Ala Ser Ser
930 935 940

~~Ile~~ Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser Tyr Asp Ala Asp
 945 950 955 960

Met Glu Val Asp Gly Phe Gln Asp Tyr Ile Asp Glu Ala Phe Asp Tyr
965 970 975

Lys Thr Glu Tyr Asp ~~Asn~~ Lys Leu Gly Asn Leu Met Asp Tyr Tyr Gly
980 985 990

Ile Lys Thr Glu Ala ~~Glu Ile~~ ~~Leu~~ Ser Gly Gly Ile Met Lys Ala Ser
 995 1000 1005

Lys Thr Phe Asp Arg Arg Lys Asp ~~Ala~~ Glu Ala Ile Ser Val Ala Val
1010 1015 1020

Arg Ala Leu Arg Lys Gln Ala Arg Ala Thr Phe Lys Arg Arg Asn Asp
1025 1030 1035 1040

Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr His Val Thr Tyr
1045 1050 1055

His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly ~~Leu~~ Lys Arg Ala His
1060 1065 1070

Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu Ile Gln Ile Lys
1075 1080 1085

Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu Ser Ser Leu Arg
1090 1095 1100

Ala Gln Leu Ser His Arg Leu Val Leu Lys
1105 1110